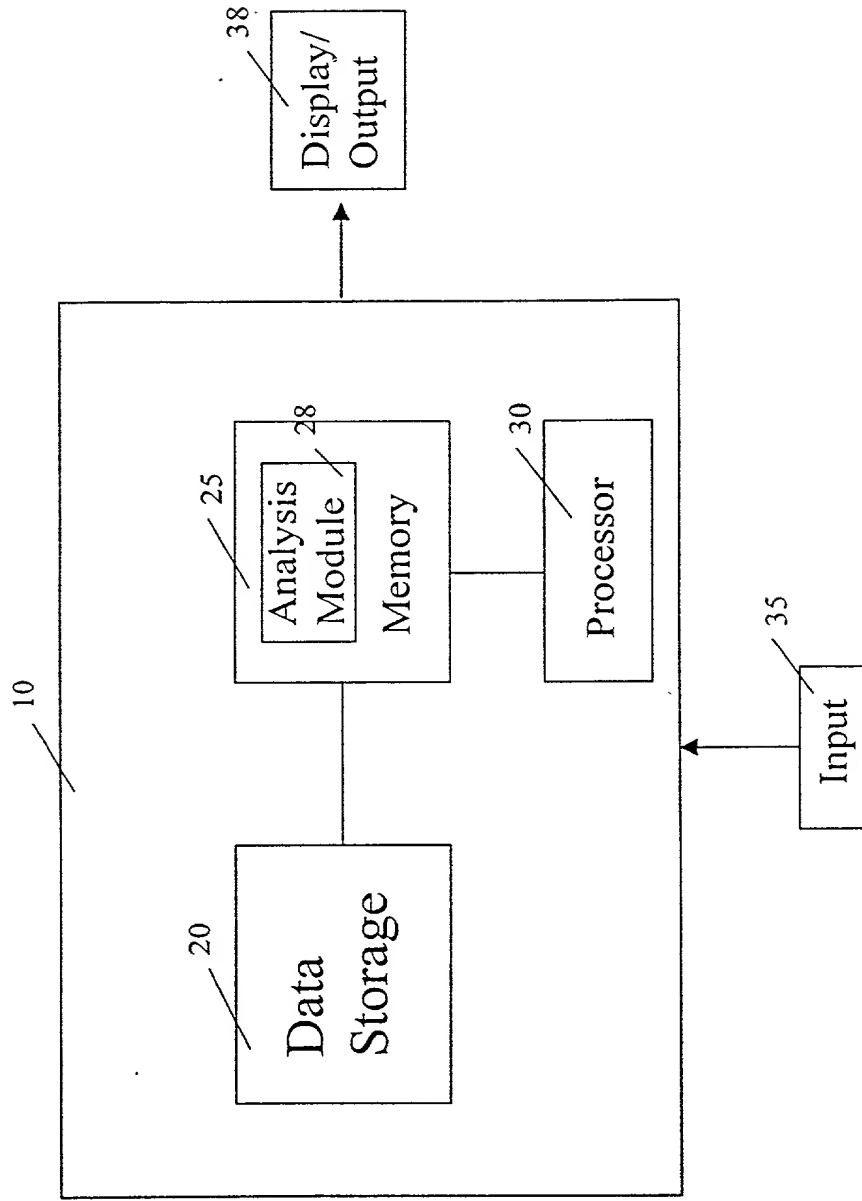


Figure 1

Figure 2



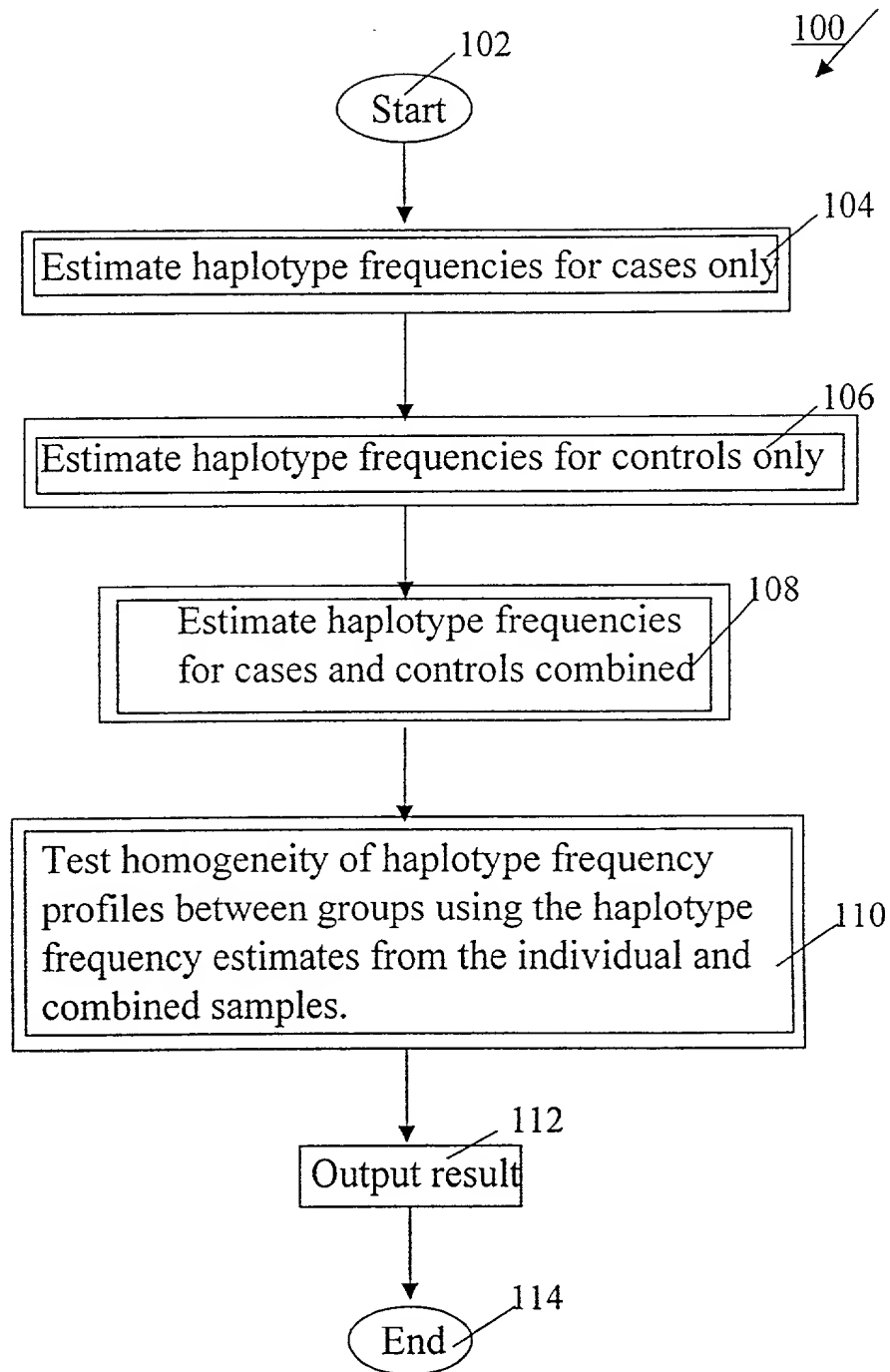


Figure 3

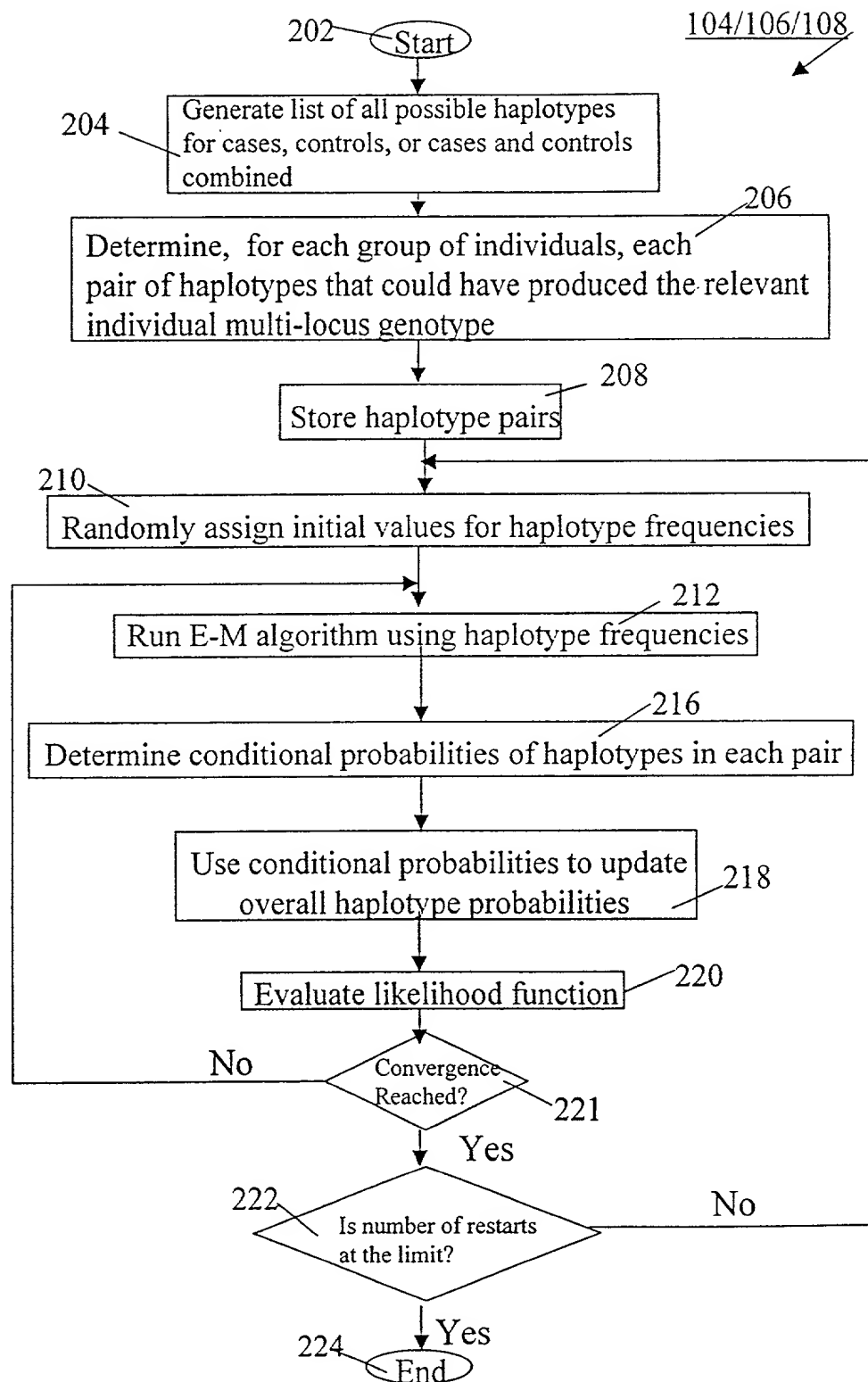


Figure 4

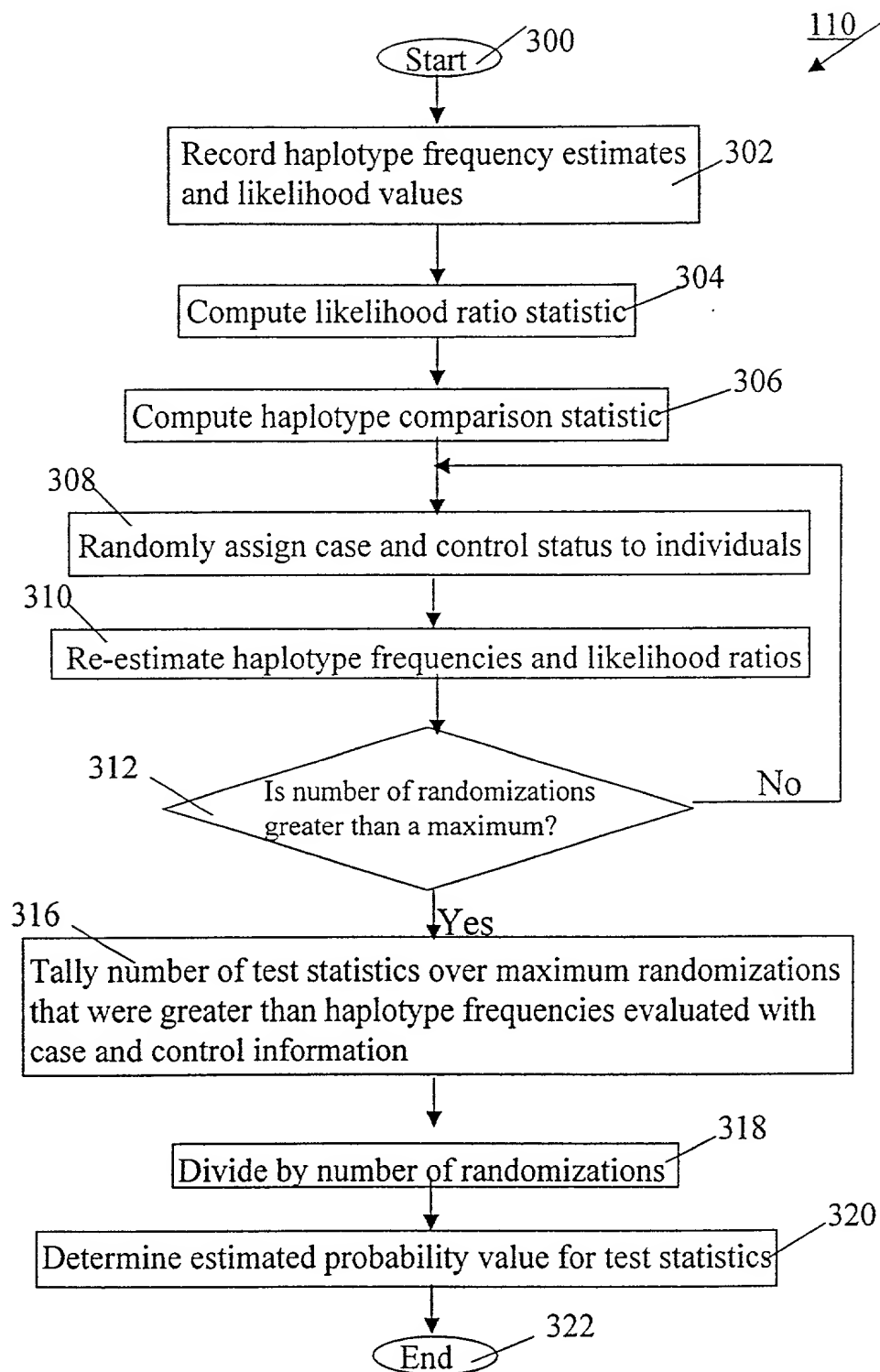


Figure 5

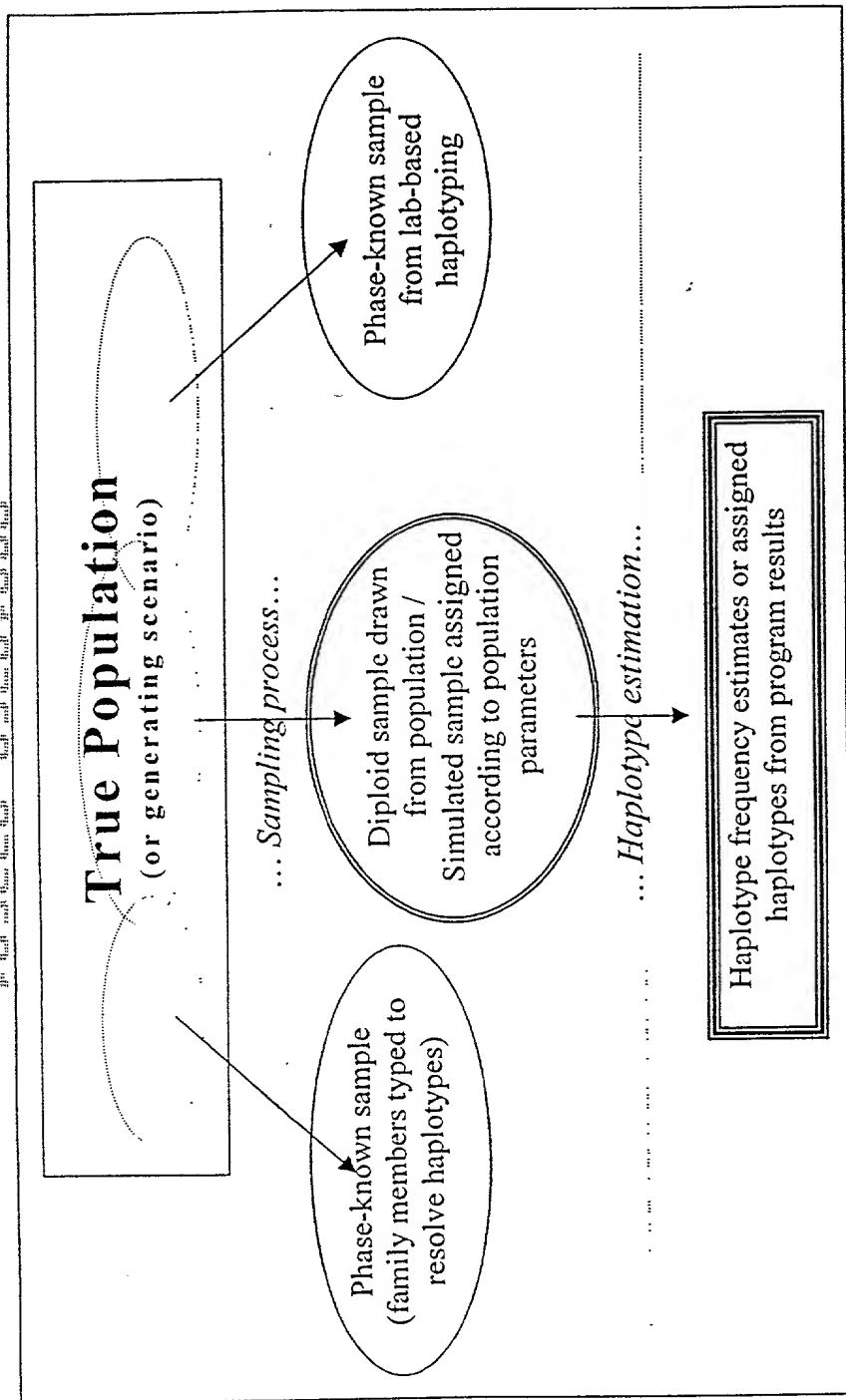


Figure 6

104920-09261560

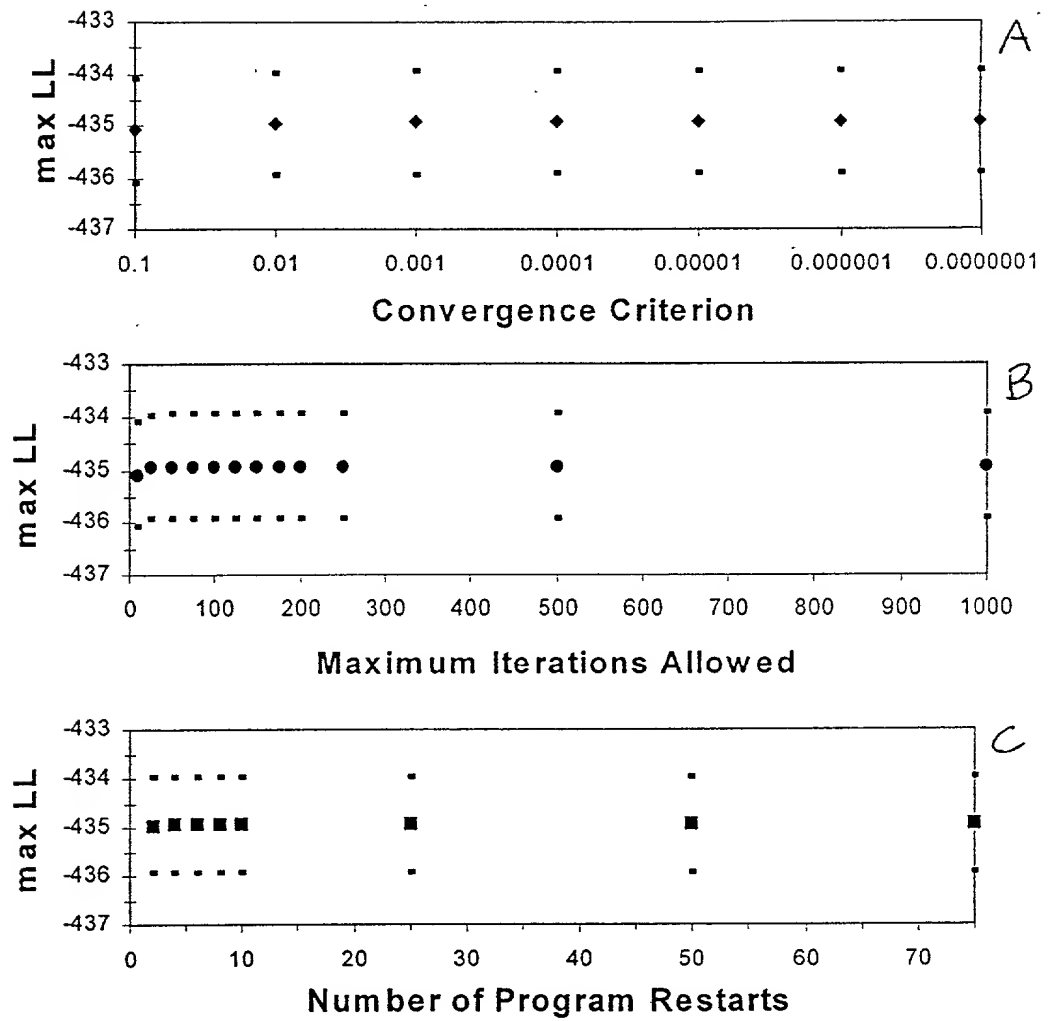


Figure 7

TO 920-0000-1800

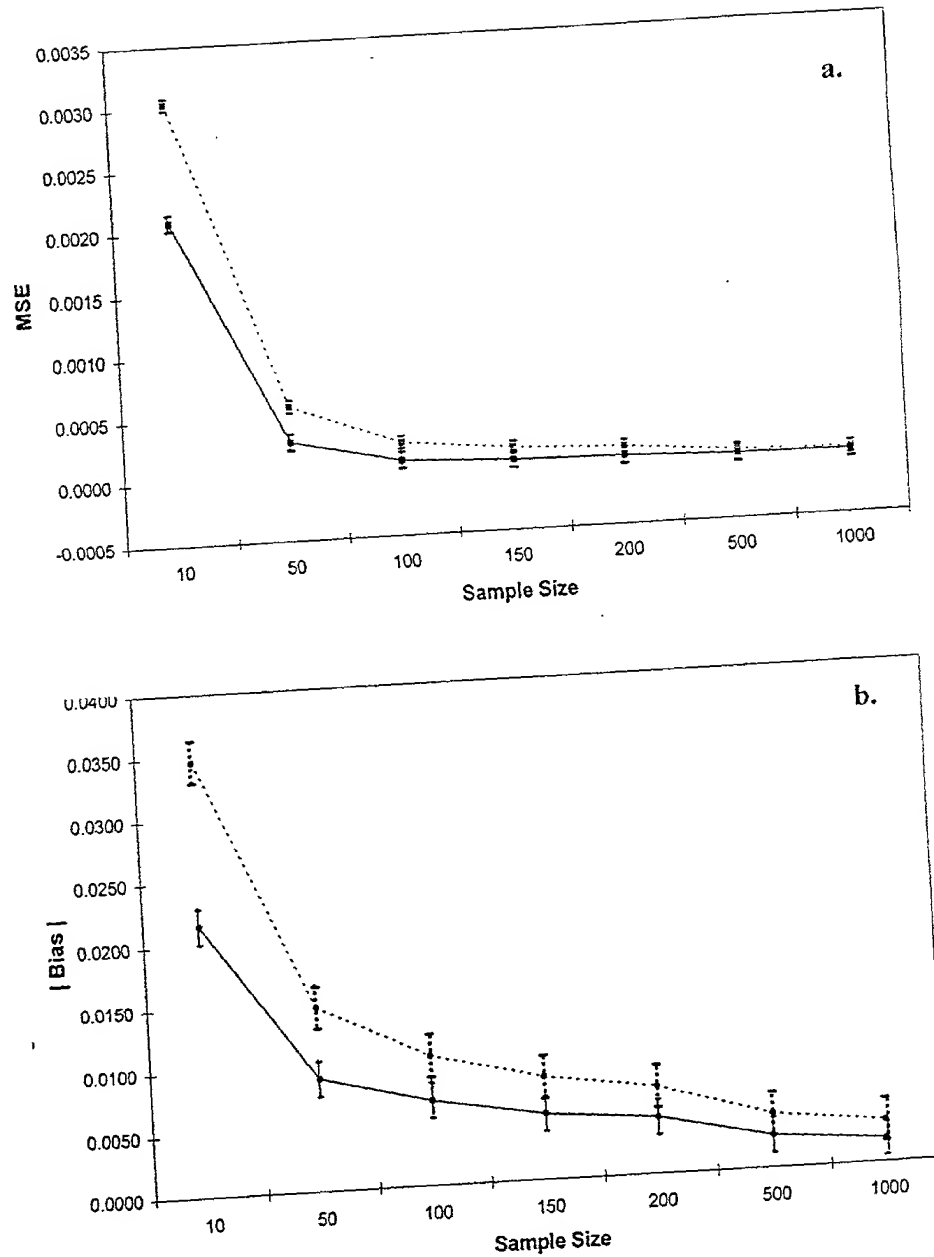


Figure 8

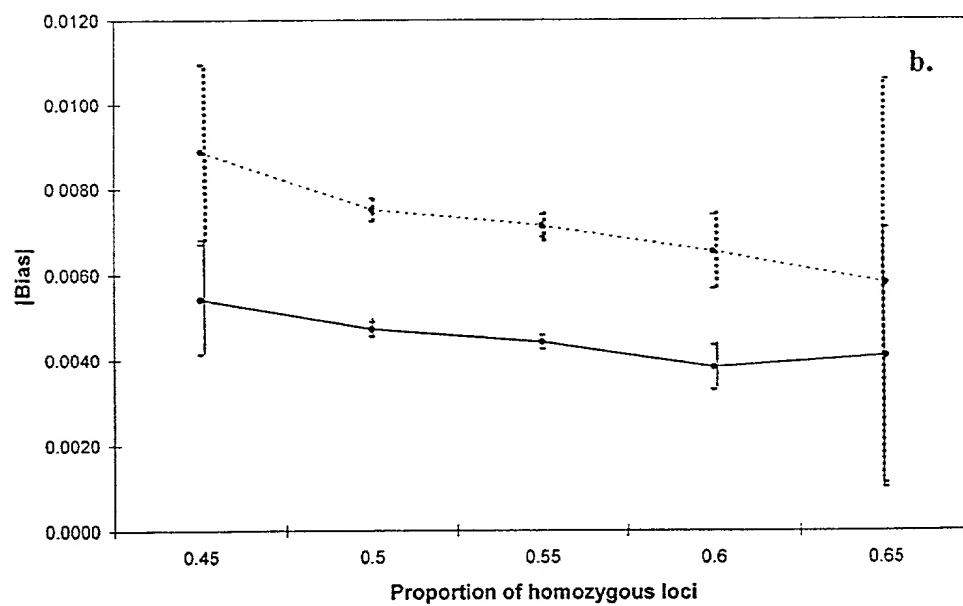
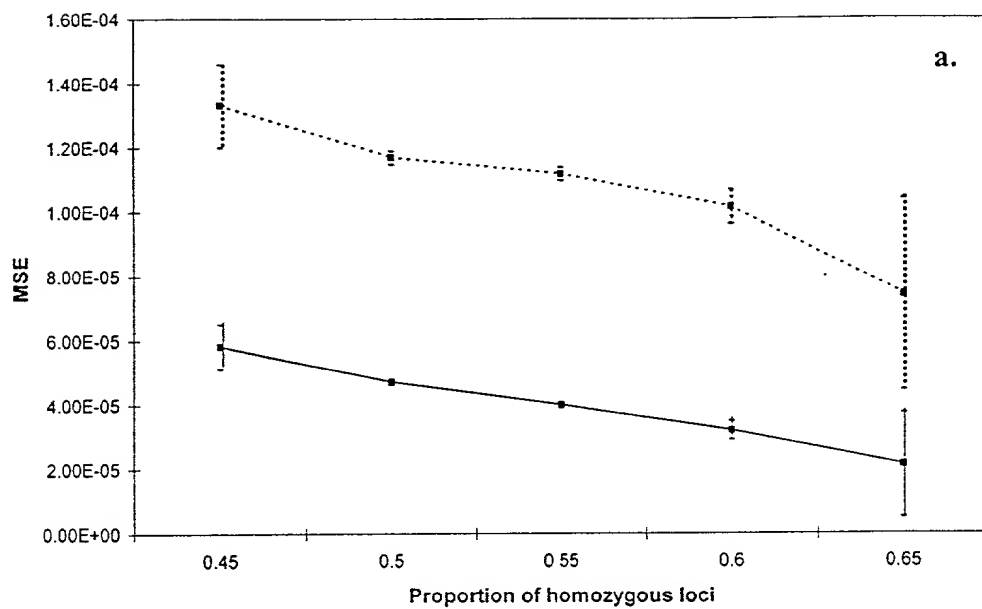


Figure 9

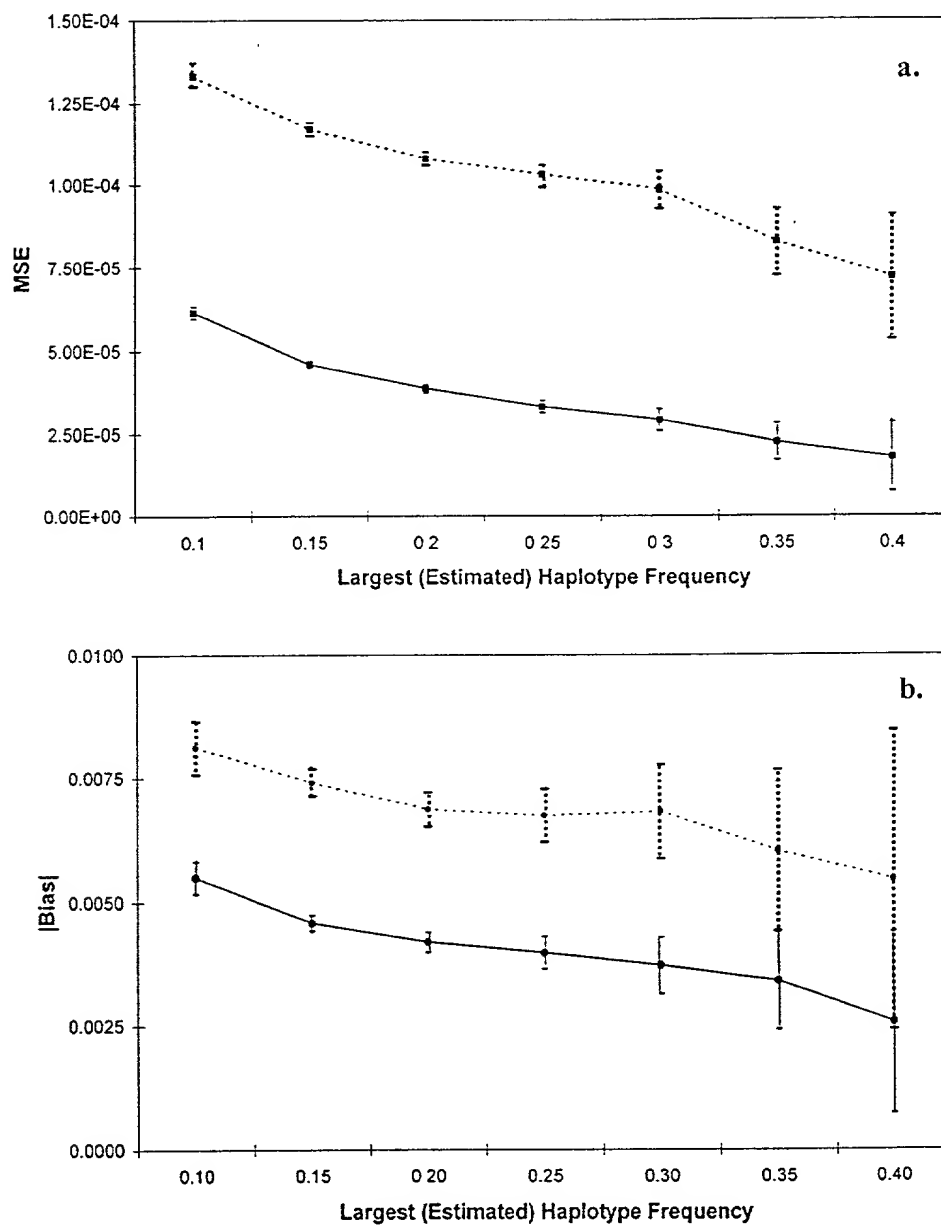


Figure 10

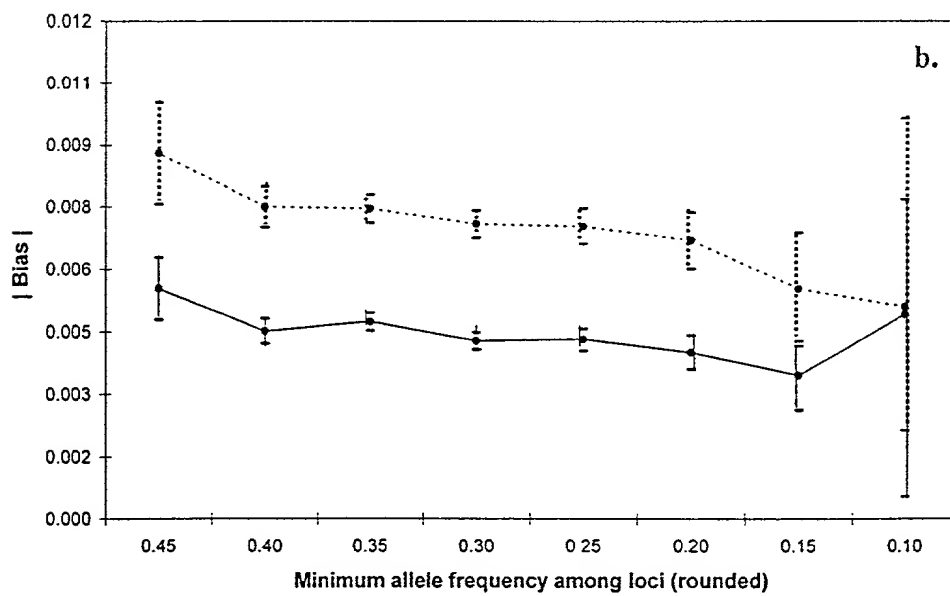
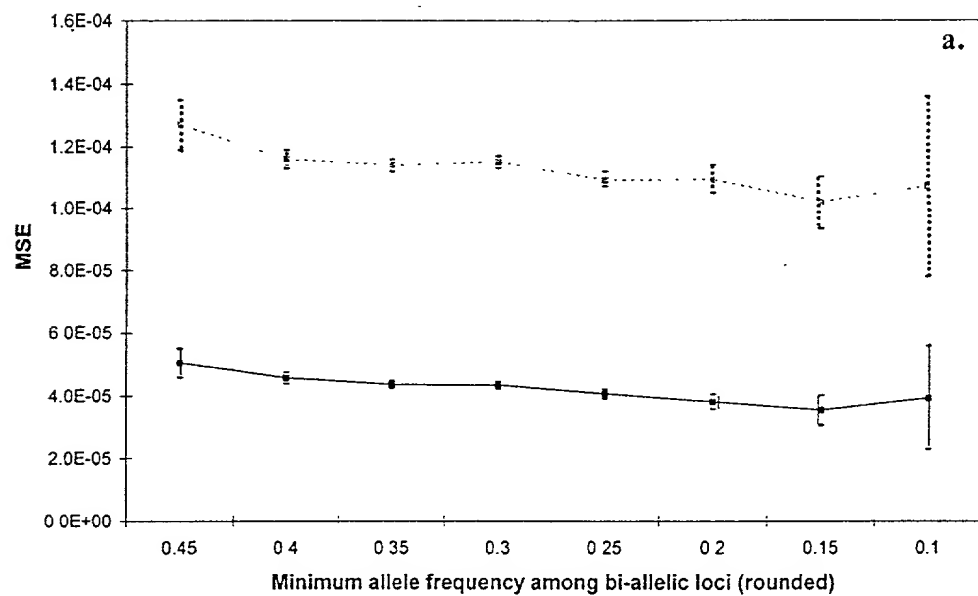


Figure 11

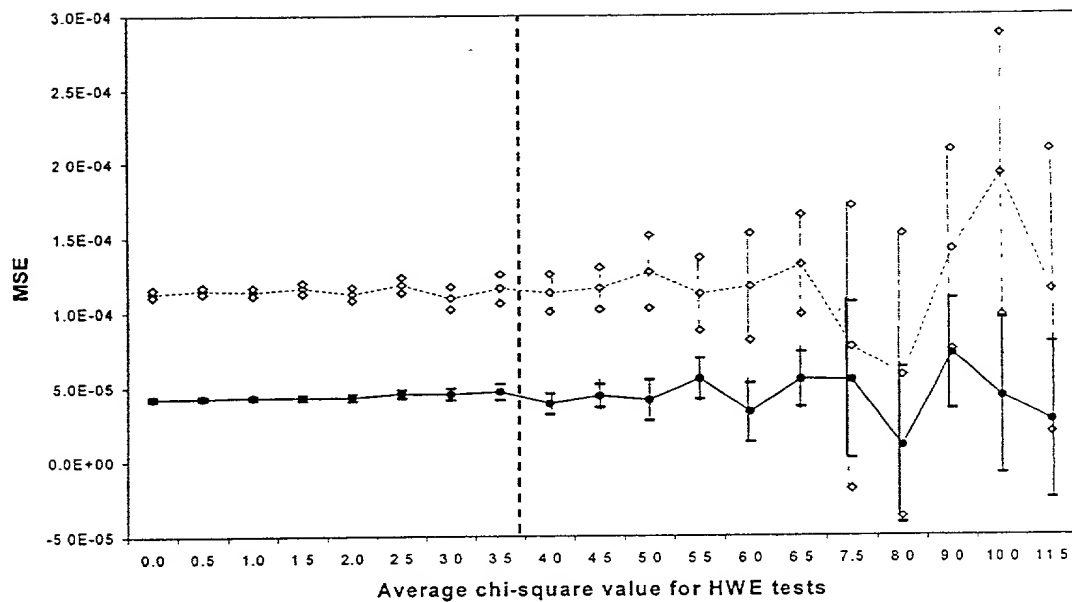


Figure 12

Figure 13 consists of two line graphs, (a) and (b), showing the effect of the number of loci on bias and NSE.

Graph (a) shows Bias (Y-axis, 0.000 to 0.016) versus Number of Loci (X-axis, 2 to 10). The solid line with circles shows a decreasing trend in bias as the number of loci increases, starting at approximately 0.0045 for 2 loci and reaching approximately 0.0025 for 10 loci. The dotted line with circles shows a relatively flat trend, starting at approximately 0.0145 for 2 loci and ending at approximately 0.0125 for 10 loci.

Graph (b) shows NSE (Y-axis, -0.00005 to 0.00040) versus Number of Loci (X-axis, 2 to 10). The solid line with circles shows an increasing trend in NSE as the number of loci increases, starting at approximately 0.00007 for 2 loci and reaching approximately 0.00035 for 10 loci. The dotted line with circles shows a relatively flat trend, starting at approximately 0.00038 for 2 loci and ending at approximately 0.00032 for 10 loci.

Figure 13

Table. Regression of absolute value of bias between estimated and generating haplotype frequencies on all factors.

Regression including all factors				Single-factor models		
Variable	Estimate	Std. Error	T test	Prob > T	R**2	F
2-locus Haplotypes:						
INTERCEP	0.031017	0.00220248	14.083	0.0001	0.0383	395.1818
Prop HOMOZ	-0.029256	0.00369778	-7.912	0.0001	0.0468	487.0159
Freq largest Hap.	-0.00238	0.00258249	-0.922	0.3568	0.0085	84.85
Chi-sq for LD	-3.0429E-05	0.00000383	-7.944	0.0001	0.0004	4.0044
H-W status	-0.000878	0.00080228	-1.094	0.274	0.0337	345.6019
Avg. Min Allele freq.	0.008471	0.00478999	1.769	0.077		
5-locus haplotypes:						
INTERCEP	0.058585	0.00499106	11.738	0.0001	0.0027	9.7079
PropHOMOZ	-0.004128	0.0033604	-1.229	0.2193	0.0085	30.2177
Freq largest Hap.	-0.007354	0.00163342	-4.502	0.0001	0.0452	166.6065
Avg D' for pairwise LD matrix	0.013172	0.00102619	12.836	0.0001	0.0002	0.8555
H-W status	-0.00155	0.00139011	-1.115	0.265	0.0001	0.3553
Avg. Min Allele freq.	-8.5172E-05	0.00038764	-0.22	0.8261		

Figure 14

Table. Haplotype Frequency Estimates and Significance Levels of Case-control Comparison from Permutation Tests

Chromosome 19 APOE Gene Region:											
Configuration 1						Configuration 2:					
M1 M2 M3 M4* M5 M6 M7 M8 → → → → → → → →						M1 M2 M3 M4* M5 M6 M7 M8 → → → → → → → →					
* part of e4 allele determination (APOEεSNP included in haplotypes)						* part of e4 allele determination (Loci included flank the APOEε4 SNP)					
Haplotype	Overall	Case	Control	χ ²	P value*	Haplotype	Overall	Case	Control	χ ²	P value*
TCCA	0.007	0.012	0.000	1.83	0.243	TACA	0.207	0.192	0.220	0.42	0.357
CCCA	0.013	0.022	0.000	3.34	0.025	CACA	0.057	0.050	0.069	0.60	0.357
TTCA	0.009	0.009	0.007	0.04	0.884	TGCA	0.015	0.003	0.034	5.53	0.002
CTCA	0.031	0.049	0.000	7.41	0.014	CGCA	0.166	0.190	0.132	2.10	0.044
TCTA	0.224	0.197	0.258	1.81	0.072	TATA	0.021	0.019	0.023	0.06	0.810
CCTA	0.198	0.189	0.219	0.47	0.285	CATA	0.005	0.009	0.004	0.27	0.776
TTTA	0.000	0.000	0.000	0.00	0.116	TGTA	0.000	0.000	0.000	0.00	0.395
CTTA	0.004	0.006	0.002	0.26	0.837	CGTA	0.008	0.009	0.008	0.02	0.896
TCCG	0.002	0.003	0.000	0.44	0.664	TACG	0.232	0.262	0.195	2.21	0.055
CCCG	0.002	0.004	0.000	0.64	0.562	CACG	0.066	0.049	0.092	2.57	0.061
TTCC	0.088	0.115	0.056	3.56	0.023	TGCG	0.013	0.000	0.032	6.67	0.000
CTCG	0.079	0.110	0.042	5.22	0.023	CGCG	0.176	0.189	0.152	0.83	0.209
TCTG	0.138	0.124	0.159	0.85	0.276	TATG	0.000	0.000	0.000	0.00	0.285
CCTG	0.180	0.135	0.228	5.01	0.008	CATG	0.018	0.014	0.022	0.33	0.606
TTTG	0.017	0.014	0.017	0.04	0.78	TGTG	0.000	0.000	0.000	0.00	0.619
CTTG	0.010	0.010	0.012	0.04	0.846	CGTG	0.016	0.015	0.018	0.05	0.804
Likelihoods:	-1117.2	-668.7	-416.9	63.12**	0.0001		-1149.7	-621.6	-511.5	33.34**	0.0041

Other Haplotype Configurations and Significance Levels			
Chromosome 19 region			
Configuration 3:	M1 M2 M3 M4* M5 M6 M7 M8	Haplotypes contain 4 locus	LRT **
Configuration 4:	M1 M2 M3 M4* M5 M6 M7 M8	"	93.66
Configuration 5:	M1 M2 M3 M4* M5 M6 M7 M8	Haplotypes flank 4 locus	57.39
Configuration 6:	M1 M2 M3 M4* M5 M6 M7 M8	Haplotypes do not contain or flank 4 locus	45.64
Configuration 7:	M1 M2 M3 M4 M5	Haplotypes in 'control' region	13.48
Configuration 8:	M1 M2 M3 M4 M5	"	17.29
			6.49

* P values based on 10000 permutations

** Likelihood ratio test statistic values for omnibus test

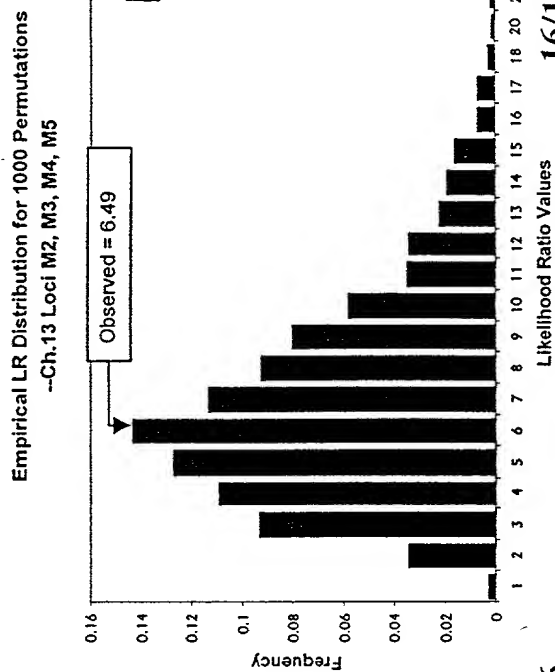
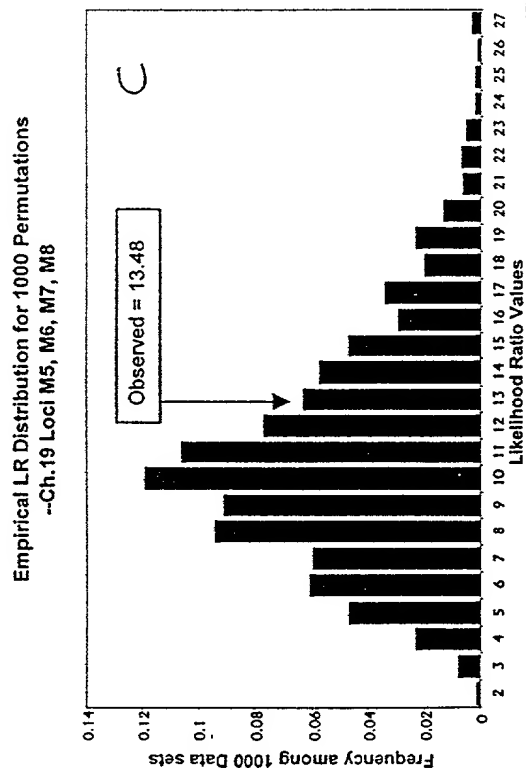
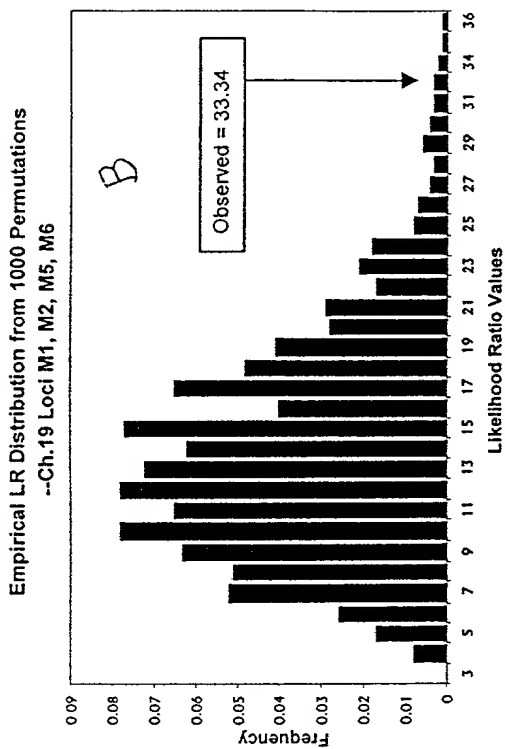
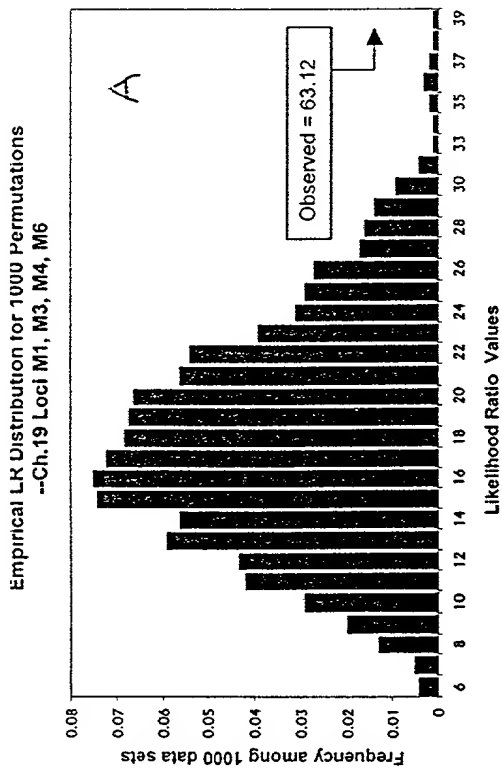


Figure 16

Haplotype Estimation Results:

Hap No.	Haplotype	MLOCUS CEPHGP	SCHORK CEPHGP	PEDIGREE CEPHGP	MLOCUS BRCAtotal	SCHORK BRCAtotal	MLOCUS BRCAcase	SCHORK BRCAcase	MLOCUS BRCAcon	SCHORK BRCAcon
1	1111111	0.29210	0.29208	0.28280	0.21030	0.21687	0.23710	0.24214	0.20470	0.20564
2	1122211	0.20090	0.20085	0.20200	0.02750	0.01921	0.02510	0.02215	0.02700	0.01695
3	1222211	0.17790	0.17793	0.17680	0.14840	0.14497	0.21270	0.20714	0.10000	0.10101
4	1212111	0.11110	0.11111	0.10610	0.21090	0.21302	0.20120	0.18571	0.21360	0.22727
5	2111121	0.09290	0.09293	0.10100	0.16570	0.16256	0.15240	0.16429	0.16630	0.15626
6	1111112	0.08590	0.08586	0.09090	0.01560	0.01479	0.00000	0.00000	0.00000	0.00000
7	1211111	0.01400	0.01399	0.01520	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000
8	1111121	0.02220	0.02222	0.02520	0.00560	0.00636	0.00000	0.00000	0.00000	0.00000
9	2111121	0.00300	0.00303	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000
10	1122111	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000
11	1111211	0.00000	0.00000	0.00000	0.18230	0.19231	0.14630	0.15714	0.20910	0.22042
12	2111111	0.00000	0.00000	0.00000	0.01870	0.01686	0.00000	0.00000	0.02630	0.02344
13	2111121	0.00000	0.00000	0.00000	0.00610	0.00608	0.00000	0.00000	0.01120	0.01041
14	1211121	0.00000	0.00000	0.00000	0.00000	0.00000	0.01220	0.00714	0.00000	0.00000
15	1222211	0.00000	0.00000	0.00000	0.00000	0.00000	0.00680	0.00786	0.00000	0.00000
16	1122211	0.00000	0.00000	0.00000	0.00000	0.00000	0.00610	0.00642	0.00000	0.00000
17	1111221	0.00000	0.00000	0.00000	0.00120	0.00150	0.00000	0.00000	0.00480	0.00000
18	2112111	0.00000	0.00000	0.00000	0.00250	0.00252	0.00000	0.00000	0.00420	0.00392
19	2112121	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00330	0.00000
20	1122121	0.00000	0.00000	0.00000	0.00260	0.00000	0.00000	0.00000	0.00130	0.00000
21	1212112	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000
22	1121212	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000
23	2111221	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000
24	1221221	0.00000	0.00000	0.00000	0.00260	0.00296	0.00000	0.00000	0.00000	0.00000
25	1111221	1.00000	1.00000	1.00000	1.00000	1.00001	0.99990	0.99999	1.00000	1.00000

Figure 17